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OIPE

RAW SEQUENCE LISTING

DATE: 08/10/2001

PATENT APPLICATION: US/09/919,770

TIME: 07:59:14

Input Set : A:\UOFW117618.txt

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3 <110> APPLICANT: Bornstein, Paul
 4 Kyriakides, Themis
 5 Ratner, Buddy
 6 Giachelli, Cecilia
 7 Martinson, Laura
 8 Scatena, Marta
 10 <120> TITLE OF INVENTION: Methods and Devices to Modulate the Wound Response
 12 <130> FILE REFERENCE: UOFW117618
 14 <140> CURRENT APPLICATION NUMBER: US/09/919,770
 14 <141> CURRENT FILING DATE: 2001-07-31
 14 <150> PRIOR APPLICATION NUMBER: US 60/222,071
 15 <151> PRIOR FILING DATE: 2000-08-01
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1469
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo Sapien
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (102)..(1001)
 30 <400> SEQUENCE: 1
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 34 Met Arg Ile Ala Val
 35 1 5
 37 att tgc ttt tgc ctc cta ggc atc acc tgt gcc ata cca gtt aaa cag 164
 38 Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala Ile Pro Val Lys Gln
 39 10 15 20
 41 gct gat tct gga agt tct gag gaa aag cag ctt tac aac aaa tac cca 212
 42 Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu Tyr Asn Lys Tyr Pro
 43 25 30 35
 45 gat gct gtg gcc aca tgg cta aac cct gac cca tot cag aag cag aat 260
 46 Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro Ser Gln Lys Gln Asn
 47 40 45 50
 49 ctc cta gcc cca cag acc ctt cca agt aag tcc aac gaa agc cat gac 308
 50 Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser Asn Glu Ser His Asp
 51 55 60 65
 53 cac atg gat gat atg gat gat gaa gat gat gat gac cat gtg gac agc 356
 54 His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His Val Asp Ser
 55 70 75 80 85
 57 cag gac tcc att gac tcg aac gac tct gat gat gta gat gac act gat 404
 58 Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp Asp Thr Asp
 59 90 95 100
 61 gat tct cac cag tct gat gag tct cac cat tct gat gaa tct gat gaa 452
 62 Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu Ser Asp Glu
 63 105 110 115

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66 Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu Val Phe Thr
67      120      125      130
69 cca gtt gtc ccc aca gta gac aca tat gat ggc cga ggt gat agt gtg      548
70 Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly Asp Ser Val
71      135      140      145
73 gtt tat gga ctg agg tca aaa tct aag aag ttt cgc aga cct gac atc      596
74 Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg Pro Asp Ile
75 150      155      160      165
77 cag tac cct gat gct aca gac gag gac atc acc tca cac atg gaa agc      644
78 Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr Ser His Met Glu Ser
79      170      175      180
81 gag gag ttg aat ggt gca tac aag gcc atc ccc gtt gcc cag gac ctg      692
82 Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala Gln Asp Leu
83      185      190      195
85 aac gcg cct tct gat tgg gac agc cgt ggg aag gac agt tat gaa acg      740
86 Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser Tyr Glu Thr
87      200      205      210
89 agt cag ctg gat gac cag agt gct gaa acc cac agc cac aag cag tcc      788
90 Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His Ser His Lys Gln Ser
91      215      220      225
93 aga tta tat aag cgg aaa gcc aat gat gag agc aat gag cat tcc gat      836
94 Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu His Ser Asp
95 230      235      240      245
97 gtg att gat agt cag gaa ctt tcc aaa gtc agc cgt gaa ttc cac agc      884
98 Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu Phe His Ser
99      250      255      260
101 cat gaa ttt cac agc cat gaa gat atg ctg gtt gta gac ccc aaa agt      932
102 His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp Pro Lys Ser
103      265      270      275
105 aag gaa gaa gat aaa cac ctg aaa ttt cgt att tct cat gaa tta gat      980
106 Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His Glu Leu Asp
107      280      285      290
109 agt gca tct tct gag gtc aat taaaaggaga aaaaatacaa tttctcactt      1031
110 Ser Ala Ser Ser Glu Val Asn
111      295      300
113 tgcatttagt caaaagaaaa aatgctttat agcaaaatga aagagaacat gaaatgcttc      1091
115 tttctcagtt tatttggttga atgtgtatct atttgagtct ggaaataact aatgtgtttg      1151
117 ataattagtt tagtttgttg cttcatggaa actccctgta aactaaaagc ttcagggtta      1211
119 tgtctatggt cattctatag aagaaatgca aactatcact gtattttaat atttgttatt      1271
121 ctctcatgaa tagaaattta tgtagaagca aacaaaatac ttttaccac ttaaaaagag      1331
123 aatataacat tttatgtcac tataatcttt tgttttttaa gttagtgtat attttgttgt      1391
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131 <211> LENGTH: 300
132 <212> TYPE: PRT
133 <213> ORGANISM: Homo Sapien
135 <400> SEQUENCE: 2

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137 Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
138 1 5 10 15
141 Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
142 20 25 30
145 Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
146 35 40 45
149 Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser
150 50 55 60
153 Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp
154 65 70 75 80
157 Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp
158 85 90 95
161 Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser
162 100 105 110
165 Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala
166 115 120 125
169 Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly
170 130 135 140
173 Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe
174 145 150 155 160
177 Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr
178 165 170 175
181 Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro
182 180 185 190
185 Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys
186 195 200 205
189 Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His
190 210 215 220
193 Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser
194 225 230 235 240
197 Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser
198 245 250 255
201 Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val
202 260 265 270
205 Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile
206 275 280 285
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214 <211> LENGTH: 5784
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216 <213> ORGANISM: Homo Sapien
218 <220> FEATURE:
219 <221> NAME/KEY: CDS
220 <222> LOCATION: (240)..(3755)
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225 cgcatataa agccgcgctg cccgggagcc gctcgccac gtccaccgga gcatcctgca 120
227 ctgcagggcc ggtctctcgc tccagcagag cctgcgcctt tctgactcgg tccggaacac 180

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229	tgaaaccagt catcactgca tcttttttggc aaaccaggag ctcagctgca ggaggcagg	239
231	atg gtc tgg agg ctg gtc ctg ctg gct ctg tgg gtg tgg ccc agc acg	287
232	Met Val Trp Arg Leu Val Leu Leu Ala Leu Trp Val Trp Pro Ser Thr	
233	1 5 10 15	
235	caa gct ggt cac cag gac aaa gac acg acc ttc gac ctt ttc agt atc	335
236	Gln Ala Gly His Gln Asp Lys Asp Thr Thr Phe Asp Leu Phe Ser Ile	
237	20 25 30	
239	agc aac atc aac cgc aag acc att ggc gcc aag cag ttc cgc ggg ccc	383
240	Ser Asn Ile Asn Arg Lys Thr Ile Gly Ala Lys Gln Phe Arg Gly Pro	
241	35 40 45	
243	gac ccc ggc gtg ccg gct tac cgc ttc gtg cgc ttt gac tac atc cca	431
244	Asp Pro Gly Val Pro Ala Tyr Arg Phe Val Arg Phe Asp Tyr Ile Pro	
245	50 55 60	
247	ccg gtg aac gca gat gac ctc agc aag atc acc aag atc atg cgg cag	479
248	Pro Val Asn Ala Asp Asp Leu Ser Lys Ile Thr Lys Ile Met Arg Gln	
249	65 70 75 80	
251	aag gag ggc ttc ttc ctc acg gcc cag ctc aag cag gac ggc aag tcc	527
252	Lys Glu Gly Phe Phe Leu Thr Ala Gln Leu Lys Gln Asp Gly Lys Ser	
253	85 90 95	
255	agg ggc acg ctg ttg gct ctg gag ggc ccc ggt ctc tcc cag agg cag	575
256	Arg Gly Thr Leu Leu Ala Leu Glu Gly Pro Gly Leu Ser Gln Arg Gln	
257	100 105 110	
259	ttc gag atc gtc tcc aac ggc ccc gcg gac acg ctg gat ctc acc tac	623
260	Phe Glu Ile Val Ser Asn Gly Pro Ala Asp Thr Leu Asp Leu Thr Tyr	
261	115 120 125	
263	tgg att gac ggc acc cgg cat gtg gtc tcc ctg gag gac gtc ggc ctg	671
264	Trp Ile Asp Gly Thr Arg His Val Val Ser Leu Glu Asp Val Gly Leu	
265	130 135 140	
267	gct gac tcg cag tgg aag aac gtc acc gtg cag gtg gct ggc gag acc	719
268	Ala Asp Ser Gln Trp Lys Asn Val Thr Val Gln Val Ala Gly Glu Thr	
269	145 150 155 160	
271	tac agc ttg cac gtg ggc tgc gac ctc ata gga cca gtt gct ctg gac	767
272	Tyr Ser Leu His Val Gly Cys Asp Leu Ile Gly Pro Val Ala Leu Asp	
273	165 170 175	
275	gag ccc ttc tac gag cac ctg cag gcg gaa aag agc cgg atg tac gtg	815
276	Glu Pro Phe Tyr Glu His Leu Gln Ala Glu Lys Ser Arg Met Tyr Val	
277	180 185 190	
279	gcc aaa ggc tct gcc aga gag agt cac ttc agg ggt ttg ctt cag aac	863
280	Ala Lys Gly Ser Ala Arg Glu Ser His Phe Arg Gly Leu Leu Gln Asn	
281	195 200 205	
283	gtc cac cta gtg ttt gaa aac tct gtg gaa gat att cta agc aag aag	911
284	Val His Leu Val Phe Glu Asn Ser Val Glu Asp Ile Leu Ser Lys Lys	
285	210 215 220	
287	ggt tgc cag caa ggc cag gga gct gag atc aac gcc atc agt gag aac	959
288	Gly Cys Gln Gln Gly Gln Gly Ala Glu Ile Asn Ala Ile Ser Glu Asn	
289	225 230 235 240	
291	aca gag acg ctg cgc ctg ggt ccg cat gtc acc acc gag tac gtg ggc	1007
292	Thr Glu Thr Leu Arg Leu Gly Pro His Val Thr Thr Glu Tyr Val Gly	
293	245 250 255	

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295	ccc	agc	tcg	gag	agg	agg	ccc	gag	gtg	tgc	gaa	cgc	tcg	tgc	gag	gag	1055
296	Pro	Ser	Ser	Glu	Arg	Arg	Pro	Glu	Val	Cys	Glu	Arg	Ser	Cys	Glu	Glu	
297				260					265					270			
299	ctg	gga	aac	atg	gtc	cag	gag	ctc	tcg	ggg	ctc	cac	gtc	ctc	gtg	aac	1103
300	Leu	Gly	Asn	Met	Val	Gln	Glu	Leu	Ser	Gly	Leu	His	Val	Leu	Val	Asn	
301			275					280						285			
303	cag	ctc	agc	gag	aac	ctc	aag	aga	gtg	tcg	aat	gat	aac	cag	ttt	ctc	1151
304	Gln	Leu	Ser	Glu	Asn	Leu	Lys	Arg	Val	Ser	Asn	Asp	Asn	Gln	Phe	Leu	
305			290					295						300			
307	tgg	gag	ctc	att	ggt	ggc	cct	cct	aag	aca	agg	aac	atg	tca	gct	tgc	1199
308	Trp	Glu	Leu	Ile	Gly	Gly	Pro	Pro	Lys	Thr	Arg	Asn	Met	Ser	Ala	Cys	
309	305					310						315				320	
311	tgg	cag	gat	ggc	cgg	ttc	ttt	gcg	gaa	aat	gaa	acg	tgg	gtg	gtg	gac	1247
312	Trp	Gln	Asp	Gly	Arg	Phe	Phe	Ala	Glu	Asn	Glu	Thr	Trp	Val	Val	Asp	
313				325							330				335		
315	agc	tgc	acc	acg	tgt	acc	tgc	aag	aaa	ttt	aaa	acc	att	tgc	cac	caa	1295
316	Ser	Cys	Thr	Thr	Cys	Thr	Cys	Lys	Lys	Phe	Lys	Thr	Ile	Cys	His	Gln	
317				340						345				350			
319	atc	acc	tgc	ccg	cct	gca	acc	tgc	gcc	agt	cca	tcc	ttt	gtg	gaa	ggc	1343
320	Ile	Thr	Cys	Pro	Pro	Ala	Thr	Cys	Ala	Ser	Pro	Ser	Phe	Val	Glu	Gly	
321			355					360						365			
323	gaa	tgc	tgc	cct	tcc	tgc	ctc	cac	tcg	gtg	gac	ggg	gag	gag	ggc	tgg	1391
324	Glu	Cys	Cys	Pro	Ser	Cys	Leu	His	Ser	Val	Asp	Gly	Glu	Glu	Gly	Trp	
325			370					375						380			
327	tct	ccg	tgg	gca	gag	tgg	acc	cag	tgc	tcc	gtg	acg	tgt	ggc	tct	ggg	1439
328	Ser	Pro	Trp	Ala	Glu	Trp	Thr	Gln	Cys	Ser	Val	Thr	Cys	Gly	Ser	Gly	
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331	acc	cag	cag	aga	ggc	cgg	tcc	tgt	gac	gtc	acc	agc	aac	acc	tgc	ttg	1487
332	Thr	Gln	Gln	Arg	Gly	Arg	Ser	Cys	Asp	Val	Thr	Ser	Asn	Thr	Cys	Leu	
333				405						410					415		
335	ggg	ccc	tcg	atc	cag	aca	cgg	gct	tgc	agt	ctg	agc	aag	tgt	gac	acc	1535
336	Gly	Pro	Ser	Ile	Gln	Thr	Arg	Ala	Cys	Ser	Leu	Ser	Lys	Cys	Asp	Thr	
337			420						425					430			
339	cgc	atc	cgg	cag	gac	ggc	ggc	tgg	agc	cac	tgg	tca	cct	tgg	tct	tca	1583
340	Arg	Ile	Arg	Gln	Asp	Gly	Gly	Trp	Ser	His	Trp	Ser	Pro	Trp	Ser	Ser	
341			435					440						445			
343	tgc	tct	gtg	acc	tgt	gga	gtt	ggc	aat	atc	aca	cgc	atc	cgt	ctc	tgc	1631
344	Cys	Ser	Val	Thr	Cys	Gly	Val	Gly	Asn	Ile	Thr	Arg	Ile	Arg	Leu	Cys	
345			450					455						460			
347	aac	tcc	cca	gtg	ccc	cag	atg	ggg	ggc	aag	aat	tgc	aaa	ggg	agt	ggc	1679
348	Asn	Ser	Pro	Val	Pro	Gln	Met	Gly	Gly	Lys	Asn	Cys	Lys	Gly	Ser	Gly	
349	465					470						475				480	
351	cgg	gag	acc	aaa	gcc	tgc	cag	ggc	gcc	cca	tgc	cca	atc	gat	ggc	cgc	1727
352	Arg	Glu	Thr	Lys	Ala	Cys	Gln	Gly	Ala	Pro	Cys	Pro	Ile	Asp	Gly	Arg	
353				485						490					495		
355	tgg	agc	ccc	tgg	tcc	ccg	tgg	tcg	gcc	tgc	act	gtc	acc	tgt	gcc	ggt	1775
356	Trp	Ser	Pro	Trp	Ser	Pro	Trp	Ser	Ala	Cys	Thr	Val	Thr	Cys	Ala	Gly	
357			500						505					510			
359	ggg	atc	cgg	gag	cgc	acc	cgg	gtc	tgc	aac	agc	cct	gag	cct	cag	tac	1823

VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date